WHAT IS CLAIMED IS:

1. A method for denaturing or separating double-stranded nucleic acid molecules, said method comprising contacting one or more double-stranded nucleic acid molecules with one or more amino acid denaturants under conditions sufficient to form single-stranded nucleic acid molecules.

2. The method of claim 1, wherein said amino acid denaturants are selected from the group consisting of one or more amino acids, derivatives, analogs thereof or combinations thereof, and one or more polyamino acids, derivatives, analogs thereof or combinations thereof.

3. The method of claim 2, wherein said polyamino acids comprise two or more amino acids or derivatives or analogs thereof.

4. The method of claim 2, wherein said amino acids are selected from the group consisting of glycine, alanine, arginine, asparagine, glutamine, isoleucine, leucine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, valine, and imidazole.

5. The method of claim 4, wherein said amino acid is glycine.

6. The method of claim 1, wherein the concentration of said amino acid denaturants ranges from about 1 mM to about 500 mM.

7. The method of claim 6, wherein said concentration ranges from about 5 mM to about 50 mM.

8. The method of claim 7, wherein said concentration is about 10 mM.

9. A method of recovering one or more desired target nucleic acid molecules from a population of nucleic acid molecules comprising:

a) contacting said population with one or more hypentylated probes, under conditions sufficient to permit said probe to

hybridize to said desired target molecules thereby forming one or more hybridized molecules; and

b) isolating said desired target nucleic acid molecules from said probes by contacting said hybridized molecules with one or more amino acid denaturants.

10. The method of claim 9, wherein said population of nucleic acid molecules is single-stranded DNA.

11. The method of claim 10, wherein said single-stranded DNA is circular.

12. The method of claim 10, wherein said single-stranded DNA is linear.

13. The method of claim 10, wherein said single-stranded DNA is selected from the group consisting of single-stranded plasmids, single-stranded cosmids, and single-stranded phagemids.

14. The method of claim 9, wherein said population of nucleic acid molecules is a cDNA library.

15. The method of claim 9, wherein said haptenylated probes are bound to a support.

16. The method of claim 15, wherein said support comprises one or more binding ligands.

17. The method of claim 16, wherein said probes are bound to said support by a ligand-hapten interaction.

18. The method of claim 9, wherein said population of nucleic acid molecules is double-stranded DNA.

19. The method of claim 18, further comprising treating said double-stranded nucleic acid molecules under conditions sufficient to render such molecules single-stranded.

20. The method of claim 19, wherein said treatment comprises contacting said double-stranded nucleic acid molecule with one or more amino acid denaturants.

21. The method of claim 19, wherein said treatment comprises degradation of one strand of said double-stranded nucleic acid molecules.

22. The method of claim 21, wherein said degradation comprises the use of Gene II protein and Exonuclease III.

23. The method of claim 9, further comprising (c) incubating said isolated desired target nucleic acid molecules under conditions sufficient to synthesize a nucleic acid molecule complementary to said desired target molecules, thereby forming double-stranded nucleic acid molecules.

24. The method of claim 23, wherein said conditions comprise the use of one or more primer nucleic acid molecules and one or more nucleotides.

25. The method of claim 24, wherein said nucleotides confer nuclease resistance to said synthesized nucleic acid molecule.

26. The method of claim 25, wherein said nucleotides are nucleotide analogs.

27. The method of claim 26, wherein said nucleotide analogs are a methylated nucleotides.

28. The method of claim 27, wherein said methylated nucleotides are 5-methyldeoxycytosine.

29. The method of claim 25, further comprising digesting said double-stranded nucleic acid molecules with one or more nuclease.

30. The method of claim 29, further comprising transforming said digested molecules into one or more host cells.

31. The method of claim 23, further comprising transforming said double-stranded molecules into one or more host cells.

32. The method of claim 9, wherein said probes are degenerate probes.

33. The method of claim 32, wherein said degenerate probes comprise one or more universal nucleotides.

34. The method of claim 33, wherein said degenerate probes comprise one or more nucleotides selected from the group consisting of dP and dK.

35. The method of claim 9, further comprising enriching for larger or full-length desired nucleic acid molecules.

36. The method of claim 35, wherein said enrichment comprises separating the desired nucleic acid molecules according to size.

37. The method of claim 36, wherein said method comprises amplifying the desired nucleic acid molecules prior to size separation.

38. The method of claim 9, wherein said probes comprise a Kozac sequence.

39. The method of claim 38, wherein said probes are degenerate probes.

40. The method of claim 32, wherein said degenerate probes are to a Kozac sequence.